



Page 1 of 7



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RAW SEQUENCE LISTING

DATE: 04/09/2002

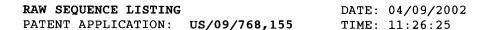
PATENT APPLICATION: US/09/768,155

TIME: 11:26:25

Input Set : N:\Crf3\RULE60\09768155.raw Output Set: N:\CRF3\04092002\1768155.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Morris Reichlin and Eugen Koren
      5
            (ii) TITLE OF INVENTION: METHOD FOR TREATMENT OF SLE
           (iii) NUMBER OF SEQUENCES: 12
      7
      q
            (iv) CORRESPONDENCE ADDRESS:
     10
                   (A) ADDRESSEE: Patrea L. Pabst
     11
                   (B) STREET: 2800 One Atlantic Center
     12
                               1201 West Peachtree Street
     13
                   (C) CITY: Atlanta
     14
                  (D) STATE: Georgia
                                                             ENTERED
     15
                   (E) COUNTRY: USA
     16
                   (F) ZIP: 30306-3450
     18
             (V) COMPUTER READABLE FORM:
     19
                   (A) MEDIUM TYPE: Floppy disk
                   (B) COMPUTER: IBM PC compatible
     20
     21.
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     22
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     24
            (vi) CURRENT APPLICATION DATA:
C--> 25
                   (A) APPLICATION NUMBER: US/09/768,155
C--> 26
                   (B) FILING DATE: 23-Jan-2001
     32
                  (C) CLASSIFICATION:
     29
           (vii) PRIOR APPLICATION DATA:
     30
                  (A) APPLICATION NUMBER: 08/800,682
     31
                  (B) FILING DATE:
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     35
                  (A) NAME: Pabst, Patrea L.
     36
                  (B) REGISTRATION NUMBER: 31,284
     37
                  (C) REFERENCE/DOCKET NUMBER: OMRF 158 CIP
     39
            (ix) TELECOMMUNICATION INFORMATION:
     40
                  (A) TELEPHONE: (404)873-8794
                  (B) TELEFAX: (404)873-8795
     41
        (2) INFORMATION FOR SEO ID NO: 1:
     43
     44
             (i) SEQUENCE CHARACTERISTICS:
     45
                  (A) LENGTH: 1314 base pairs
     46
                  (B) TYPE: nucleic acid
     47
                  (C) STRANDEDNESS: single
     48
                  (D) TOPOLOGY: linear
W--> 49
            (ii) MOLECULE TYPE: DNA
     50
           (iii) HYPOTHETICAL: NO
     51
            (iv) ANTI-SENSE: NO
     52
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     54 GGTGAAGAAG GAGTTGTGCC AGCACGTGAG TACTCAGACG ATCGTAACAT CAACCTGGCA
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Input Set : N:\Crf3\RULE60\09768155.raw
Output Set: N:\CRF3\04092002\I768155.raw

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56 GACGAATTAA AAATTGGTGA TACCATTGAA GCAGTTGTCA TTTCTAACGT AACAAGCGAC
                                                                        120
58 AAGGAAGGCG TCAGTTACTT GTTGTCAAAG AAGCGTTTGG ATGCGCGCAA GGCATGGGAA
                                                                        180
60 AACTTGAGCT TTGCTGAAGG TGACACAGTT GATGCCAAGG TTATCAACGC TGTTCGTGGT
                                                                        240
62 GGTTTGATTG TTGATGTTAA CGGCGTACGT GGTTTCGTAC CAGCATCAAT GGTTGCAGAA
                                                                        300
64 CGTTTCGTTT CTGATTTGAA CCAATTCAAG AATAAGGATA TTAAAGCACA AGTTATCGAA
                                                                        360
66 ATTGACCCTG CTAATGCACG TTTGATTTTG TCACGTAAGG CTGTTGCTGC ACAAGAACGC
                                                                        420
68 GCTGCACGAT TGGCTGAAGT ATTTAGCAAG TTGTCAGTTC GTGAAGTTGT TGAAGGAACT
                                                                        480
540
72 CACGTATCAG AAATCTCACA CGATCGTGTG AAGAACCCGG CCGATGTATT GACAAAGGGT
                                                                        600
74 GACAAGGTTG ATGTTAAGAT CTTGGCATTG GACACTGAAA AGGGTCGTAT CTCATTGTCA
                                                                        660
76 ATCAAAGCAA CACAACGTGG ACCTTGGGAC GAAGCTGCAG ATCAAATCGC TGCAGGTTCA
78 GTGCTTGAAG GTACTGTTAA GCGTGTGAAG GACTTTGGTG CCTTTGTTGA AATTTTGCCT
                                                                        780
80 GGTATCGAAG GTCTTGTGCA CGTGTCACAA ATTTCAAACA AGCGTATTGA AAACCCATCA
                                                                        840
82 GAAGTTTTGA AGTCTGGTGA CAAGGTACAA GTGAAGGTAT TGGACATTAA GCCAGCCGAA
                                                                        900
84 GAACGTATTT CATTGTCAAT GAAGGCTTTG GAAGAAAAGC CAGAACGTGA AGATCGTCGT
                                                                        960
86 GGTAACGATG GTTCAGCTTC ACGTGCTGAT ATCGCTGCTT ACAAGCAACA AGATGACTCA
                                                                       1020
88 GCCGCAACAT TGGGTGACAT CTTTGGTGAT AAGTTGTAAG AGGCATCAAC ATAAAAGAGC
                                                                       1080
90 TGGTTCGCCA GTTCTTTTAT TTTTGAAGAA AAATTGAGTG GGCATTAGTG GGCGCTCACG
                                                                       1140
92 GTATGAAAAA GGAGGTGCGA TTATGGCAGC ACCAGTAGTA GCCATTGTTG GCGACCAAAC
                                                                       1200
94 GTCGGAAAAT CGACTATCTT TAACCGGATG GCCGGAGAAC GTATTGCAAT TGTTGAAGAT
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96 CAACCAGGGG TAACACGCGA TCGTTTGTAC GCGCCAGCCG AATGGTTGAA TTAT
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98 (2) INFORMATION FOR SEQ ID NO: 2:
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100
              (A) LENGTH: 352 amino acids
101
              (B) TYPE: amino acid
102
              (C) STRANDEDNESS: single
103
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: protein
104
       (iii) HYPOTHETICAL: NO
105
106
       (iv) ANTI-SENSE: NO
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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109 Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg Asn
110 1
                    5
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112 Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu Ala Val
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                                    25
115 Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser Tyr Leu Leu
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118 Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu Asn Leu Ser Phe
119
                            55 -
                                                60
121 Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val Arg Gly
                        70
                                            75
124 Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro Ala Ser
125
                    85
127 Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys Asn Lys
128
                                    105
                100
                                                       110
130 Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala Arg Leu
           115
                               120
133 Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala Gln Leu
                           135
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RAW SEQUENCE LISTING DATE: 04/09/2002 PATENT APPLICATION: US/09/768,155 TIME: 11:26:25

Input Set : N:\Crf3\RULE60\09768155.raw
Output Set: N:\CRF3\04092002\1768155.raw

	Ala 145	Glu	Val	Phe	Ser	Lys 150	Leu	Ser	Val	Gly	Glu 155	Val	Val	Glu	Gly	Thr 160
		Ala	Arg	Leu	Thr		Phe	Gly	Ala	Phe		Asp	Leu	Gly	Gly	
140					165					170					175	
	Asp	Gly	Leu		His	Val	Ser	Glu		Ser	His	Asp	Arg		Lys	Asn
143	Dro	71 -	7 an	180	Tou	mh.~	T	C1	185	T ***	37-1	2	17-1	190	т1 о	т о
145	PIO	Ala	195		ьеи	THE	гуѕ	200	ASP	гуѕ	vaı	ASP	205	ьуs	шe	Leu
	Ala	Leu			Glu	Lys	Gly		Ile	Ser	Leu	Ser		Lys	Ala	Thr
149		210	-			•	215					220		•		
		Arg	Gly	Pro	${\tt Trp}$		Glu	Ala	Ala	Asp		Ile	Ala	Ala	Gly	
	225					230					235					240
	Val	Leu	Glu	Gly		Val	Lys	Arg	Val		Asp	Phe	Gly	Ala	Phe	Val
155					245					250					255	
	Glu	Ile	Leu		Gly	Ile	Glu	Gly		Val	His	Val	Ser		Ile	Ser
158				260					265					270		
	Asn	Lys		Ile	Glu	Asn	Pro		Glu	Val	Leu	Lys	Ser	Gly	Asp	Lys
161	_		275		_			280					285			
	Val	Gln	Val	Lys	Val	Leu		Ile	Lys	Pro	Ala		Glu	Arg	Ile	Ser
164	T	290	.	*		- .	295	a 1	-	_	a 1	300	~1	_	_	_
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		3		01	a		a	.	- 1 -		315	- 1		_	_	320
	GIĀ	Asn	Asp	GTÀ		Ата	ser	Arg	Ala	_	Пе	Ala	Ala	Tyr		Gln
170	Cln	Asp	7 an	Con	325	7 J a	m h ~	Tan	C1	330	т1.	Dha	C1	100	335	T 0
173	GIII	кэр	АЗР	340	нта	нта	1111	ьеu	345	ASP	TIE	Pile	GIY	350	гуѕ	ьеu
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176	(2)				CE CE											
177		(~)			ENGTH					ds						
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179				-	RANI				ıle							
180					POLC			_								
181		(ii)	MOI	ECUI	E TY	PE:	prot	ein								
182	((iii)	HYE	POTHE	ETICA	L: N	10									
183		(iv)	ANT	I-SE	ENSE:	NO										•
184					E DE											
		Phe	Ala	Glu	_	Asp	Thr	Val	Asp		Lys	Val	Ile	Asn	Ala	Val
187			_		5	_		,_		10					15	
		Gly														Pro
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	АТа	Ser		Val	Ala	GLu	Arg		Val	Ser	Asp	Leu		Gln	Phe	Lys
193	7 an	Trra	35	т1а	T	7 T -	Cl n	40	т1.	C1.	т1.	3 ~~	45	7 1 a	3	7 1 m
196	ASII	Lys 50	азр	тте	nys	НТG	55	val	тте	GIU	тте	Asp 60	PLO	ATG	ASN	нта
	Ara	Leu	Tle	T.eu	Ser	Ara		Δla	Va1	Δla	Δla		Glu	Δrσ	Δla	Δla
199		Leu		20Cu	561	70	-12	.114	* UL I	nzu	75	3111	JIU	A	лта	80
		Leu	Ala	Glu	Val		Ser	Lvs	Leu	Ser		G] v	Glu	Va1	Va 1	
202					85			-10		90		1		,	95	
	Gly	Thr	Val	Ala		Leu	Thr	Asp	Phe		Ala	Phe	Val	Asp		Gly
	_				-			-		-				-		-

RAW SEQUENCE LISTINGPATENT APPLICATION: US/09/768,155

DATE: 04/09/2002
TIME: 11:26:25

Input Set : N:\Crf3\RULE60\09768155.raw
Output Set: N:\CRF3\04092002\1768155.raw

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205		17-1	N a n	100	Т о ч	17a l	TT i a	37.0.1	105	~1	т1-	a	TT -	110	3	**- 7
207		Val	115	СТУ	Leu	Val	птѕ	120	ser	GIU	тте	ser		ASP	Arg	vaı
		λen		λΊэ	λan	1751	T 011		Tvva	C1	7	T	125	3 ~~	17.0 1	T
211		Asn 130	PIO	мта	ASP	Val	135	TIIT	цуs	СТУ	ASP		Val	ASP	val	rys
			7 1 n	T 011	7 00	mh ~		T	C1	3	т1.	140	+	a	-1 -	-
		Leu	нта	reu	ASP		GIU	ьуѕ	GIY	Arg		ser	ьeu	ser	шe	
	145	mh m	C1 -	7	01	150	m	.	a 1	31	155		a 1	- 1		160
217	нта	Thr	GIII	ALG		PLO	ттр	ASP	GIU		Ala	Asp	GIN	TTE		Ата
	c1	0	37- 7	T	165	01	m 1	77 - 1	T	170	77- 1			-,	175	
219	GTĀ	Ser	Val		GIU	GLY	Thr	vaı		Arg	vaı	Lys	Asp		GTĀ	Ala
220	nha	17 n 1	a 1	180	T	D	a 1	+1 -	185	01	-			190	_	
	Pile	Val		тте	ьeu	Pro	GIY		GIU	GIY	Leu	vaı		vaı	Ser	GIn
223	т1.	a	195	T	3	-1 -	a 1	200	.		a 1		205	_	_	
	тте	Ser	ASI	гàг	Arg	тте		Asn	Pro	ser	GLu		Leu	Lys	Ser	GLY
226	7 ~~	210	77 - 1	a 1	11- 1	T	215	-		-1	_	220		~ 7		_
		Lys	vaı	GIn	val		vaı		Asp	шe		Pro	Ala	Glu	Glu	-
	225	a	.		30.1	230		_	~ 1	~ 1	235	_		_		240
	ire	Ser	Leu	Ser		Lys	Ala	Leu	GLu		Lys	Pro	Glu	Arg		
232					245					250					255	
	(2)	INFO														
235		(1)		QUEN						_						
236				A) LI					acio	is						
237				3) TY												
238			((C) Si	l'RANI	DEDNI	ESS:	sind	те							
~ ~ ~									•							
239) T(ear	•							
240			MOI	LECUI	E TY	PE:	pro	ear								
240 241		(iii)	MOI HYI	LECUI POTHI	LE TY	PE: L: 1	pro	ear	,							
240 241 242		(iii) (iv)	MOI HYH ANI	LECUI POTHI FI-SI	LE TY ETICA ENSE:	PE: AL: 1 NO	prof	ear tein								
240 241 242 243	ı	(iii) (iv) (xi)	MOI HYI ANT	LECUI POTHI FI-SI QUENC	LE TY ETICA ENSE: CE DA	PE: AL: 1 NO ESCRI	prof 10 [PTI	ear tein ON: S	SEQ]							
240 241 242 243 245	Ala	(iii) (iv)	MOI HYI ANT	LECUI POTHI FI-SI QUENC	LE TY ETICA ENSE: CE DI Ala	PE: AL: 1 NO ESCRI	prof 10 [PTI	ear tein ON: S	SEQ]	Gly			Asn	Gly		Val
240 241 242 243 245 246	Ala 1	(iii) (iv) (xi) Tyr	MOI HYI ANT SEQ Glu	LECUI POTHI TI-SI QUENC ASP	ETICA ENSE: CE DA Ala 5	YPE: AL: 1 : NO ESCRI Glu	prof NO IPTIC Thr	ear tein ON: S Val	SEQ I	Gly 10	Val	Ile			15	
240 241 242 243 245 246 248	Ala 1	(iii) (iv) (xi)	MOI HYI ANT SEQ Glu	LECUI POTHI FI-SI QUENC ASP	ETICA ENSE: CE DA Ala 5	YPE: AL: 1 : NO ESCRI Glu	prof NO IPTIC Thr	ear tein ON: S Val	SEQ I Thr Asp	Gly 10	Val	Ile		Phe	15	
240 241 242 243 245 246 248 249	Ala 1 Lys	(iii) (iv) (xi) Tyr Gly	MOI HYI ANI SE(Glu	LECUI POTHI FI-SI QUENC ASP Phe 20	ETICA ENSE: CE DI Ala 5 Thr	(PE: AL: NO: SCRI Glu Val	prof NO IPTIO Thr Glu	ear tein ON: S Val Leu	SEQ I Thr Asp 25	Gly 10 Gly	Val Ile	Ile Arg	Ala	Phe 30	15 Leu	Pro
240 241 242 243 245 246 248 249 251	Ala 1 Lys	(iii) (iv) (xi) Tyr	MOI HYI ANT SEC Glu Gly Leu	LECUI POTHI FI-SI QUENC ASP Phe 20	ETICA ENSE: CE DI Ala 5 Thr	(PE: AL: NO: SCRI Glu Val	prof NO IPTIO Thr Glu	ear tein ON: S Val Leu	SEQ I Thr Asp 25	Gly 10 Gly	Val Ile	Ile Arg	Ala Leu	Phe 30	15 Leu	Pro
240 241 242 243 245 246 248 249 251 252	Ala 1 Lys Gly	(iii) (iv) (xi) Tyr Gly Ser	MOI HYI ANT SEQ Glu Gly Leu 35	ECUI POTHI FI-SI QUENC Asp Phe 20 Val	LE TY ETICA ENSE: CE DA Ala 5 Thr	VPE: AL: NO ESCRI Glu Val	prof NO IPTIC Thr Glu Arg	ear tein ON: S Val Leu Pro 40	SEQ Thr Asp 25 Val	Gly 10 Gly Arg	Val Ile Asp	Ile Arg Thr	Ala Leu 45	Phe 30 His	15 Leu Leu	Pro Glu
240 241 242 243 245 246 248 249 251 252 254	Ala 1 Lys Gly	(iii) (iv) (xi) Tyr Gly Ser	MOI HYI ANT SEQ Glu Gly Leu 35	ECUI POTHI FI-SI QUENC Asp Phe 20 Val	LE TY ETICA ENSE: CE DA Ala 5 Thr	VPE: AL: NO ESCRI Glu Val	prof NO IPTIC Thr Glu Arg	ear tein ON: S Val Leu Pro 40	SEQ Thr Asp 25 Val	Gly 10 Gly Arg	Val Ile Asp	Ile Arg Thr Asp	Ala Leu 45	Phe 30 His	15 Leu Leu	Pro Glu
240 241 242 243 245 246 248 249 251 252 254 255	Ala 1 Lys Gly	(iii) (iv) (xi) Tyr Gly Ser Lys 50	MOI HYI ANT SEQ Glu Gly Leu 35 Glu	POTHE FI-SE QUENC Asp Phe 20 Val	ETICA ENSE: CE DH Ala 5 Thr Asp	YPE: AL: NO ESCRI Glu Val Val Phe	prof NO IPTIC Thr Glu Arg Lys 55	ON: S Val Leu Pro 40 Val	SEQ Thr Asp 25 Val	Gly 10 Gly Arg Lys	Val Ile Asp Leu	Ile Arg Thr Asp 60	Ala Leu 45 Gln	Phe 30 His	15 Leu Leu Arg	Pro Glu Asn
240 241 242 243 245 246 248 249 251 252 254 255 257	Ala 1 Lys Gly Gly Asn	(iii) (iv) (xi) Tyr Gly Ser	MOI HYI ANT SEQ Glu Gly Leu 35 Glu	POTHE FI-SE QUENC Asp Phe 20 Val	ETICA ENSE: CE DH Ala 5 Thr Asp	YPE: AL: NO ESCRI Glu Val Val Phe Arg	prof NO IPTIC Thr Glu Arg Lys 55	ON: S Val Leu Pro 40 Val	SEQ Thr Asp 25 Val	Gly 10 Gly Arg Lys	Val Ile Asp Leu Glu	Ile Arg Thr Asp 60	Ala Leu 45 Gln	Phe 30 His	15 Leu Leu Arg	Pro Glu Asn Ala
240 241 242 243 245 246 248 249 251 252 254 255 257 258	Ala 1 Lys Gly Gly Asn 65	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val	MOI HYI ANT SEC Glu Gly Leu 35 Glu Val	POTHIFIELD ASP Phe 20 Val Leu Val	LE TY ETICA ENSE: CE DE Ala 5 Thr Asp Glu Ser	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70	Prof NO LPTIC Thr Glu Arg Lys 55 Arg	Pro 40 Val	SEQ Thr Asp 25 Val Ile	Gly 10 Gly Arg Lys Ile	Val Ile Asp Leu Glu 75	Ile Arg Thr Asp 60 Ser	Ala Leu 45 Gln Glu	Phe 30 His Lys Asn	15 Leu Leu Arg Ser	Pro Glu Asn Ala 80
240 241 242 243 245 246 248 249 251 252 254 255 257 258 260	Ala 1 Lys Gly Gly Asn 65	(iii) (iv) (xi) Tyr Gly Ser Lys 50	MOI HYI ANT SEC Glu Gly Leu 35 Glu Val	POTHIFIELD ASP Phe 20 Val Leu Val	LE TY ETICA ENSE: CE DA Ala 5 Thr Asp Glu Ser Leu	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70	Prof NO LPTIC Thr Glu Arg Lys 55 Arg	Pro 40 Val	SEQ Thr Asp 25 Val Ile	Gly 10 Gly Arg Lys Ile Gln	Val Ile Asp Leu Glu 75	Ile Arg Thr Asp 60 Ser	Ala Leu 45 Gln Glu	Phe 30 His Lys Asn	15 Leu Leu Arg Ser Val	Pro Glu Asn Ala 80
240 241 242 243 245 246 248 249 251 252 254 255 257 258 260 261	Ala 1 Lys Gly Gly Asn 65 Glu	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val	MOI HYI ANT SEC Glu Gly Leu 35 Glu Val	POTHIFIELD POTHIFIELD PASP Phe 20 Val Leu Val	LE TY ETICA ENSE: CE DE Ala 5 Thr Asp Glu Ser Leu 85	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg	DN: S Val Leu Pro 40 Val Ala	SEQ Thr Asp 25 Val Ile Val	Gly 10 Gly Arg Lys Ile Gln 90	Val Ile Asp Leu Glu 75 Glu	Ile Arg Thr Asp 60 Ser Gly	Ala Leu 45 Gln Glu Met	Phe 30 His Lys Asn Glu	15 Leu Leu Arg Ser Val 95	Pro Glu Asn Ala 80 Lys
240 241 242 243 245 246 248 249 251 252 254 255 257 260 261 263	Ala 1 Lys Gly Gly Asn 65 Glu	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val	MOI HYI ANT SEC Glu Gly Leu 35 Glu Val	POTHIFIT-SI QUENC Asp Phe 20 Val Leu Val Gln	LE TY ETICA ENSE: CE DE Ala 5 Thr Asp Glu Ser Leu 85	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg	DN: S Val Leu Pro 40 Val Ala	SEQ Thr Asp 25 Val Ile Val Leu	Gly 10 Gly Arg Lys Ile Gln 90	Val Ile Asp Leu Glu 75 Glu	Ile Arg Thr Asp 60 Ser Gly	Ala Leu 45 Gln Glu Met	Phe 30 His Lys Asn Glu Asp	15 Leu Leu Arg Ser Val 95	Pro Glu Asn Ala 80 Lys
240 241 242 243 245 246 248 249 251 252 254 255 260 261 263 264	Ala 1 Lys Gly Gly Asn 65 Glu	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val Arg	MOI HYI ANT SEC Glu Gly Leu 35 Glu Val Asp	POTHIFIT-SIQUENCE Asp Phe 20 Val Leu Val Gln Lys 100	LE TY ETICA ENSE: CE DH Ala 5 Thr Asp Glu Ser Leu 85 Asn	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr	DN: S Val Leu Pro 40 Val Ala Asn	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105	Gly 10 Gly Arg Lys Ile Gln 90 Gly	Val Ile Asp Leu Glu 75 Glu Ala	Ile Arg Thr Asp 60 Ser Gly Phe	Ala Leu 45 Gln Glu Met	Phe 30 His Lys Asn Glu Asp 110	15 Leu Leu Arg Ser Val 95 Leu	Pro Glu Asn Ala 80 Lys Gly
240 241 242 243 245 246 248 249 251 252 254 255 257 258 260 261 263 264 266	Ala 1 Lys Gly Gly Asn 65 Glu	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val	MOI HYI AND SEQ Glu Gly Leu 35 Glu Val Asp	POTHIFIT-SIQUENCE Asp Phe 20 Val Leu Val Gln Lys 100	LE TY ETICA ENSE: CE DH Ala 5 Thr Asp Glu Ser Leu 85 Asn	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr	DN: S Val Leu Pro 40 Val Ala Asn Asp	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105	Gly 10 Gly Arg Lys Ile Gln 90 Gly	Val Ile Asp Leu Glu 75 Glu Ala	Ile Arg Thr Asp 60 Ser Gly Phe	Ala Leu 45 Gln Glu Met Val Trp	Phe 30 His Lys Asn Glu Asp 110	15 Leu Leu Arg Ser Val 95 Leu	Pro Glu Asn Ala 80 Lys Gly
240 241 242 243 245 246 248 249 251 252 254 255 260 261 263 264 266 267	Ala 1 Lys Gly Gly Asn 65 Glu Gly	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val Arg Ile Val	MOI HYI AND SEQ Glu Gly Leu 35 Glu Val Asp Val Asp	POTHIFIT-SIQUENCE ASP Phe 20 Val Leu Val Gln Lys 100 Gly	LE TY ETICA ENSE: CE DA Ala 5 Thr Asp Glu Ser Leu 85 Asn Leu	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr	DN: S Val Leu Pro 40 Val Ala Asn Asp Ile 120	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105 Thr	Gly 10 Gly Arg Lys Ile Gln 90 Gly Asp	Val Ile Asp Leu Glu 75 Glu Ala Met	Ile Arg Thr Asp 60 Ser Gly Phe Ala	Ala Leu 45 Gln Glu Met Val Trp 125	Phe 30 His Lys Asn Glu Asp 110 Lys	15 Leu Leu Arg Ser Val 95 Leu Arg	Pro Glu Asn Ala 80 Lys Gly Val
240 241 242 243 245 246 248 249 251 252 254 255 260 261 263 264 266 267 269	Ala 1 Lys Gly Gly Asn 65 Glu Gly	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val Arg Ile Val His	MOI HYI AND SEQ Glu Gly Leu 35 Glu Val Asp Val Asp	POTHIFIT-SIQUENCE ASP Phe 20 Val Leu Val Gln Lys 100 Gly	LE TY ETICA ENSE: CE DA Ala 5 Thr Asp Glu Ser Leu 85 Asn Leu	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr His	DN: S Val Leu Pro 40 Val Ala Asn Asp Ile 120	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105 Thr	Gly 10 Gly Arg Lys Ile Gln 90 Gly Asp	Val Ile Asp Leu Glu 75 Glu Ala Met	Ile Arg Thr Asp 60 Ser Gly Phe Ala Glu	Ala Leu 45 Gln Glu Met Val Trp 125	Phe 30 His Lys Asn Glu Asp 110 Lys	15 Leu Leu Arg Ser Val 95 Leu Arg	Pro Glu Asn Ala 80 Lys Gly Val
240 241 242 243 245 246 248 249 251 252 254 255 260 261 263 264 266 267 269 270	Ala 1 Lys Gly Gly Asn 65 Glu Gly Gly	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val Arg Ile Val His 130	MOI HYI AND SEQ Glu Gly Leu 35 Glu Val Asp Val Asp 115 Pro	POTHE FI-SE QUENC Asp Phe 20 Val Leu Val Gln Lys 100 Gly Ser	ETICATION SET OF ALA SP Glu Ser Leu 85 Asn Leu Glu	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu Leu Ile	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr His Val	DN: S Val Leu Pro 40 Val Ala Asn Asp Ile 120 Asn	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105 Thr	Gly 10 Gly Arg Lys Ile Gln 90 Gly Asp	Val Ile Asp Leu Glu 75 Glu Ala Met Asp	Ile Arg Thr Asp 60 Ser Gly Phe Ala Glu 140	Ala Leu 45 Gln Glu Met Val Trp 125 Ile	Phe 30 His Lys Asn Glu Asp 110 Lys	15 Leu Leu Arg Ser Val 95 Leu Arg	Pro Glu Asn Ala 80 Lys Gly Val Lys
240 241 242 243 245 246 248 249 251 252 254 255 260 261 263 264 266 267 269 270	Ala 1 Lys Gly Gly Asn 65 Glu Gly Gly Lys	(iii) (iv) (xi) Tyr Gly Ser Lys 50 Val Arg Ile Val His	MOI HYI AND SEQ Glu Gly Leu 35 Glu Val Asp Val Asp 115 Pro	POTHE FI-SE QUENC Asp Phe 20 Val Leu Val Gln Lys 100 Gly Ser	ETICATION SET OF ALA SP Glu Ser Leu 85 Asn Leu Glu	YPE: AL: NO ESCRI Glu Val Val Phe Arg 70 Leu Leu Leu Ile	Prof NO IPTIC Thr Glu Arg Lys 55 Arg Glu Thr His Val	DN: S Val Leu Pro 40 Val Ala Asn Asp Ile 120 Asn	SEQ Thr Asp 25 Val Ile Val Leu Tyr 105 Thr	Gly 10 Gly Arg Lys Ile Gln 90 Gly Asp	Val Ile Asp Leu Glu 75 Glu Ala Met Asp	Ile Arg Thr Asp 60 Ser Gly Phe Ala Glu 140	Ala Leu 45 Gln Glu Met Val Trp 125 Ile	Phe 30 His Lys Asn Glu Asp 110 Lys	15 Leu Leu Arg Ser Val 95 Leu Arg	Pro Glu Asn Ala 80 Lys Gly Val Lys

RAW SEQUENCE LISTING DATE: 04/09/2002 PATENT APPLICATION: US/09/768,155 TIME: 11:26:25

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Output Set: N:\CRF3\04092002\1768155.raw

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275 Gln Leu Gly Glu Asp Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu
276
                    165
                                         170
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278 Gly Thr Lys Leu Thr Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys
                                     185
281 Phe Val Glu Ile Glu Glu Gly Val Glu Gly Leu Val His Val Ser Glu
            195
                                 200
284 Met Arg Asp Arg Val Glu Asp Ala Thr Leu Val Leu Ser Val Gly Asp
                            215
287 Glu Val Glu Ala Lys Phe Thr Gly Val Asp Arg Lys Asn Arg Ala Ile
288 225
                        230
                                            235
290 Ser Leu Ser Val Arg Ala Lys Asp Glu Ala Asp Glu Lys Asp
                    245
294 (2) INFORMATION FOR SEQ ID NO: 5:
295
         (i) SEQUENCE CHARACTERISTICS:
296
              (A) LENGTH: 247 amino acids
297
              (B) TYPE: amino acid
298
              (C) STRANDEDNESS: single
299
              (D) TOPOLOGY: linear
300
        (ii) MOLECULE TYPE: protein
301
       (iii) HYPOTHETICAL: NO
302
        (iv) ANTI-SENSE: NO
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
303
305 Lys Phe Glu Ala Gly Glu Arg Val Glu Gly Ile Ile Phe Asn Gln Val
306 1
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308 Lys Gly Gly Phe Thr Val Asp Leu Asp Gly Ala Val Ala Phe Leu Pro
                20
                                    25
311 Arg Ser Gln Val Asp Ile Arg Pro Ile Arg Asp Val Thr Pro Ala Asp
314 Ala Gln Pro Ala Ala Leu Arg Asn Leu Lys Met Asp Lys Arg Arg Gly
318 Asn Ile Val Val Ser Arg Arg Thr Val Leu Glu Glu Ser Arg Ala Glu
319 65
                        70
321 Gln Arg Ser Glu Ile Val Gln Asn Leu Glu Glu Gly Gln Val Val Glu
324 Gly Val Val Lys Asn Ile Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
                100
                                    105
327 Gly Ile Asp Gly Leu Leu His Val Thr Asp Met Ala Trp Arg Arg Val
            115
                                120
                                                     125
330 Lys His Pro Ser Glu Ile Gln Asn Ile Gly Gln Gln Val Lys Val Gln
        130
                            135
333 Ile Ile Arg Ile Asn Gln Glu Thr His Arg Ile Ser Leu Gly Met Lys
                        150
                                             155
336 Gln Leu Glu Ser Asp Pro Trp Asp Gly Ile Gly Ala Lys Tyr Pro Val
                                         170
339 Gly Lys Lys Ile Ser Gly Thr Val Thr Asn Ile Thr Asp Tyr Gly Ala
340
                180
                                    185
                                                         190
342 Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Glu
                                200
346 Met Asn Arg Pro Gly Glu Gln Val Ile Glu Glu Phe Asn Lys Gly Asp
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VERIFICATION SUMMARY

DATE: 04/09/2002

PATENT APPLICATION: US/09/768,155

TIME: 11:26:26

Input Set : N:\Crf3\RULE60\09768155.raw Output Set: N:\CRF3\04092002\I768155.raw

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L:49 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1